EV334001697US

DATE: June 17, 2003

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EXPRESS MAIL CERTIFICATION

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Atty. Docket No.	Serial Number	Description	Atty.	Fee
UCSF-127CON	10/072,047	Restriction Election	PJS	
STAN-184	09/839,590	Transmittal, Amendment After Final Rejection	FPB	
PALX-007	09/408,690	Transmittal, Amendment After Final Rejection	FPB	

6-19-3

6P 3618

EXPRESS MAIL: EV334001697US		
Restriction Election	Attorney Docket No.	UCSF127CON
	Confirmation No.	3618
	First Named Inventor	D. Cox
Address to:	Application Number	10/072,047
Assistant Commissioner for Patents	Filing Date	February 8, 2002
Washington, D.C. 20231	Group Art Unit	1634
	Examiner Name	J. Fredman
	Title: Mismatch Repair Detection	

Sir:

This amendment is responsive to the Restriction Requirement dated May 20, 2003 for which a one-month period for response was given.

Please amend the application as follows:

IN THE CLAIMS

1-26. (canceled)

27. (previously added) A method of detecting a mismatch in any of a plurality of DNA duplexes of distinct nucleic acid sequence, said duplexes formed in a single hybridization reaction, comprising:

detecting, for any of said duplexes, an alteration in a bacterial cell characteristic, said alteration effected by the *in vivo* mismatch corepair of a marker that is present together with said duplex in a vector within said bacterial cell, said corepair being initiated by a mismatch in said duplex.

28. (previously added) The method of claim 27, wherein said plurality includes duplexes of at least 10 distinct nucleic acid sequences.

29. (previously added) The method of claim 28, wherein said plurality includes at least 100 duplexes of distinct nucleic acid sequence.

30. (previously added) The method of claim 29, wherein said plurality includes at least 10,000 duplexes of distinct nucleic acid sequence.

31. (previously added) The method of claim 29, wherein said plurality includes at least 100,000 duplexes of distinct nucleic acid sequence.

32. (previously added) The method of claim 27, wherein said plurality includes nucleic acid sequences derived from a prokaryote.

33. (previously added) The method of claim 27, wherein said plurality includes nucleic acid sequences derived from a virus.

34. (previously added) The method of claim 27, wherein said plurality includes nucleic acid sequences derived from a eukaryote.

35. (previously added) The method of claim 34, wherein said eukaryote is a mammal.

36. (previously added) The method of claim 35, wherein said mammal is a human.

37. (previously added) The method of claim 36, wherein said plurality includes nucleic acid sequences derived from the coding region of a human gene.

38. (previously added) The method of claim 37, wherein said human gene is selected from the group consisting of: hemoglobin, dystrophin, BRCA1, BRCA2, CFTR, factor VIII, factor IX, oncogenes, tumor suppressors, and genes on human chromosome 21.

39. (previously added) The method of claim 27, wherein said mismatch in said duplex is a single nucleotide polymorphism.

40. (previously added) The method of claim 27, wherein said marker is inactivated by said *in vivo* mismatch corepair.

41. (previously added) The method of claim 27, wherein said marker is a recombinase.

42. (previously added) The method of claim 41, wherein said recombinase is Cre recombinase.

43. (previously added) The method of claim 27, wherein said bacterial cell characteristic is selected from the group consisting of: cell color, luminescence, antibiotic sensitivity, and antibiotic resistance.

44. (previously added) The method of claim 41, wherein mismatch corepair of said recombinase alters said bacterial cell's antibiotic resistance or sensitivity.

45. (previously added) The method of claim 27, further comprising the antecedent step of forming said plurality of DNA duplexes by annealing first nucleic acid strands, said first strands including at least one nucleic acid sequence, to second nucleic acid strands, said second strands including a plurality of distinct nucleic acid sequences.

46. (previously added) The method of claim 45, wherein said plurality of second nucleic acid

strands are derived from a common source.

47. (previously added) The method of claim 46, wherein said common source is genomic DNA from a single individual.

48. (previously added) The method of claim 46, wherein said common source is cDNA from a single individual.

49. (previously added) The method of claim 45, wherein said plurality of second nucleic acid strands are derived from a pooled source.

50. (previously added) The method of claim 49, wherein said source is pooled from family members.

51. (withdrawn) A kit for detecting a mismatch in any of a plurality of DNA duplexes of distinct nucleic acid sequence, comprising:

a first vector and a second vector, each such vector including an origin suitable for replication in a bacterial cell and a sequence that encodes a marker, said first and second vector marker encoding sequences differing from one another, said sequence difference capable of undergoing but not initiating in vivo mismatch repair.

52. (withdrawn) A bacterial host cell strain for detecting a mismatch in any of a plurality of DNA duplexes of distinct nucleic acid sequence, said host strain capable of mismatch repair and having an antibiotic marker cassette flanked by recombination sites.

REMARKS

Claims 27-52 are pending, claims 51-52 have been withdrawn from consideration. Allowance of Claims 27-50 is requested.

In view of the Restriction Requirement, Applicants elect the invention of Group I without traverse.

CONCLUSION

Applicants submit that all of the claims are now in condition for allowance, which action is requested. If the Examiner finds that a Telephone Conference would expedite the prosecution of this application, she is invited to telephone the undersigned at the number provided.

The Commissioner is hereby authorized to charge any other fees under 37 C.F.R. §§ 1.16 and 1.17 which may be required by this paper, or to credit any overpayment, to Deposit Account No. 50-0815, order number UCSF-127CON.

Respectfully submitted,

Date: June 17, 2003

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